BEST AVAILABLE COPY

OIPE

RAW SEQUENCE LISTING DATE: 07/20/2001 PATENT APPLICATION: US/09/899,303 TIME: 11:23:22

Input Set : N:\Crf3\RULE60\09899303.txt Output Set: N:\CRF3\07202001\1899303.raw

SEQUENCE LISTING 4 (1) GENERAL INFORMATION:

7

8

9

14

17

19

21

25

26

28

39

44

45

50

(i) APPLICANT: MAERTENS, GEERT

BOSMAN, FONS

DE MARTYNOFF, GUY BUYSE, MARIE-ANGE

11 (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE 12

PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

ENTERED

- (iii) NUMBER OF SEQUENCES: 111
- 16 (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
- 18 (B) STREET: 1100 NORTH GLEBE ROAD
 - (C) CITY: ARLINGTON
- 20 (D) STATE: VIRGINIA
 - (E) COUNTRY: U.S.A.
- 22 (F) ZIP: 22201-4714
- 24 (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
- 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- 32 (vi) CURRENT APPLICATION DATA:
- C--> 33 (A) APPLICATION NUMBER: US/09/899,303
- C-->34(B) FILING DATE: 06-Jul-2001
 - 41 (C) CLASSIFICATION:
 - 38 (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/612,973
 - 40 (B) FILING DATE: 11-MAR-1996
 - 43 (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BYRNE, THOMAS E.
 - (B) REGISTRATION NUMBER: 32,205
 - 46 (C) REFERENCE/DOCKET NUMBER: 1487-10
 - 48 (ix) TELECOMMUNICATION INFORMATION: 49
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100
 - 54 (2) INFORMATION FOR SEQ ID NO: 1:
 - 56 (i) SEQUENCE CHARACTERISTICS:
 - 57 (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - 58 59 (C) STRANDEDNESS: single
 - 60
 - (D) TOPOLOGY: linear 62 (ii) MOLECULE TYPE: cDNA
 - 64 (iii) HYPOTHETICAL: NO
- C--> 66 (iv) ANTI-SENSE: NO
 - 71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 - 73 GGCATGCAAG CTTAATTAAT T
 - 75 (2) INFORMATION FOR SEQ ID NO: 2:

21



RAW SEQUENCE LISTING DATE: 07/20/2001 PATENT APPLICATION: US/09/899,303 TIME: 11:23:22

	77		(i)	SEQ	UENC	E CH	ARAC'	TERI	STIC	S:								
	78			(A) LE	NGTH	: 68	bas	e pa	irs								
	79			(B) TY	PE: 1	nucl	eic	acid									
	80			(C) ST	RAND	EDNE	SS:	sing	le								
	81			(D) TO	POLO	GY:	line	ar									
	83		(ii)	MOL	ECUL	E TY	PE:	CDNA										
	85	(iii)	HYP	OTHE:	TICA:	L: No	0										
:>	87		(iv)	ANT	I-SE	NSE:	NO											
	91		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	: 2:						
	93												CACC	ATCA	CT A	ATAG'	TTAAT	60
	95	TAAC	TGCA															68
	97	(2)	INFO	RMAT:	ION !	FOR S	SEQ :	ID N	0: 3	:								
	99	` '							STIC									
	100		` _ ,						ase		s							
	101								aci									
	102			•	•				sin									
	103							lin		,								
	105		(ii	•	•			CDN										
	107				POTH													
:>			-	-	ri-si													
	112		•	•	ATUR													
	113		,	•	A) N		KEY:	CDS										
	114			-	-			1	639			•						
	116		(ix	•	ATURI													
	117		(•			KEY:	mat	_pept	tide								
	118			-	-			1										
	121		(xi		•				ON: S	SEO	TD NO	0: 3	:					
		ATG	•	•										тта	CTG	TCC	TGT	48
		Met																
	125			1	-1-	5					10					15	-1-	
		CTG	ACC	АТТ	CCA	_	TCC	GCT	тат	GAG		CGC	AAC	GTG	TCC		ATG	96
		Leu																
•	129				20				-1-	25		5			30	1		
		TAC	САТ	GTC		AAC	GAC	TGC	TCC		TCA	AGC	ATT	GTG		GAG	GCA	144
		Tyr																
	133	_		35				0,10	40					45	-1-			
		GCG	GAC		ATC	ATG	CAC	ACC		GGG	TGC	GTG	CCC		G ጥ	CGG	GAG	192
		Ala																
	137		50					55		1	-1-		60	-1-	,	5		
		AAC		тст	TCC	CGC	TGC		GTA	GCG	CTC	ACC		ACG	CTC	GCA	GCT	240
		Asn																
	141					5	70					75					80	
		AGG	AAC	GCC	AGC	GTC		ACC	ACG	ACA	АТА		CGC	CAC	GTC	GAT		288
		Arg																200
	145	_				85	0		~		90	9	9			95		
		CTC	GTT	GGG	GCG		GСT	СТС	ጥርጥ	ፐርር		ΑΤС	тас	GTG	GGG		СТС	336
		Leu																550
	149			~~1	100				010	105			-1-		110			
		TGC	GGA	тст		TTC	СТС	GTC	TCC		CTG	TTC	ACC	ATC		ССТ	CGC	384

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,303

ATE: 07/20/2001 TIME: 11:23:22

152	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Glr	Ľeu	Phe	Thr	Ile	Ser	Pro	Arg		
153 155 (ccc	Cam	115					120			ma>		125					420
155 (A ra	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC		432
156 <i>I</i> 157	n1 9	130	GIU	Thr	vaı	GIn		Cys	Asn	Cys	ser		Tyr	Pro	GIA	HIS		
	א ידי א		CCM	010			135	maa	a	3.00	1 mc	140		шаа	maa	aam		400
159 A	בוד בוד	Th.~	Class	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	AIG	AAC	TGG	TCG	CCT		480
160 I 161 I	145	T 11.T	GTA	HIS	Arg		Ala	Trp	Asp	met		мет	ASN	Trp	Ser			
163 A		A C C	CCC	CMC	CMC	150	тĆС	CAC	CTC	Cm _C	155	» ma	001	<i>-</i>	aam	160		E 2 0
164 T	hr	Thr	7 3 m	Tou	OTO:	:/a1	Ser	Gln	LAU	Lau	V TO	TIO	CCA	CAA	GCT	GTC		528
165		- 111	7-4	L eu	165	, uı	001	0111	ыcu	170	ary	116	PIO	GIII	175-			
167 G		GAĆ	ATG	GTG		GGG	GCC	САТ	TGG		GTC	CTG	cce-	"كاناد.			_	570
168 v	al	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Glv	Va.l-	كانات	Ala	G1y	Leu	Ala		
169		•		180					185		, , ,			190				
171 T	'AC	TAT	TCC	ATG	GTG	GGG	AAC.	T05		AAG	GTT	TTG	ATT	GTG	ATG	CTA		624
172 т	'yr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu		
173			195	, ·	"			200					205					
175 C	TC	TTT	GCT	CTC	TAAT	AG											•	642
176 L	eu	Phe	Ala	Leu														
177		210					•											
180 (2)												•					
182		(i)	SEQ							_								
183								nino	acio	is								
184							o ac											
185			(D) TC	POLC	GY:	line	ear										
187		•	MOL				-	ein		- N	S. 4.							
189		(xi)	SEC	UENC	CE DE	SCRI	PTIC	cein ON: S					Lon	Lou	Ser	Cve		
189 191 M	let.	(xi)	SEC	UENC	E DE Ser	SCRI	PTIC	cein ON: S		Leu			Leu	Leu		Cys		
189 191 M 192	let 1	(xi) Pro	SEQ Gly	UENC Cys	E DE Ser 5	SCRI Phe	PTIC	ein ON: S Ile	Phe	Leu 10	Leu	Ala			15			
189 191 M 192 194 L	let 1	(xi) Pro	SEQ Gly	UENC Cys Pro	E DE Ser 5	SCRI Phe	PTIC	ein ON: S Ile	Phe Glu	Leu 10	Leu	Ala		Ser	15			
189 191 M 192 194 L 195	let 1 Jeu	(xi) Pro Thr	SEQ Gly Ile	UENC Cys Pro 20	Ser 5 Ala	SCRI Phe Ser	Ser Ala	ein ON: S Ile Tyr	Phe Glu 25	Leu 10 Val	Leu Arg	Ala Asn	Val	Ser 30	15 Gly	Met		
189 191 M 192 194 L 195 197 T	let 1 Jeu	(xi) Pro Thr	SEQ Gly Ile Val	UENC Cys Pro 20	Ser 5 Ala	SCRI Phe Ser	Ser Ala	ein ON: S Ile Tyr Ser	Phe Glu 25	Leu 10 Val	Leu Arg	Ala Asn	Val	Ser 30	15 Gly	Met		
189 191 M 192 194 L 195 197 T 198	let 1 Leu	(xi) Pro Thr His	SEQ Gly Ile Val 35	UENC Cys Pro 20 Thr	Ser Ser 5 Ala Asn	SCRI Phe Ser Asp	Ser Ala Cys	Tyr Ser 40	Phe Glu 25 Asn	Leu 10 Val Ser	Leu Arg Ser	Ala Asn Ile	Val Val 45	Ser 30 Tyr	15 Gly Glu	Met Ala		
189 191 M 192 194 L 195 197 T 198 200 A	let 1 Leu	(xi) Pro Thr His	SEQ Gly Ile Val 35	UENC Cys Pro 20 Thr	Ser Ser 5 Ala Asn	SCRI Phe Ser Asp	Ser Ala Cys	Tyr Ser 40	Phe Glu 25 Asn	Leu 10 Val Ser	Leu Arg Ser	Ala Asn Ile	Val Val 45	Ser 30 Tyr	15 Gly Glu	Met Ala		
189 191 M 192 194 L 195 197 T 198 200 A 201	let 1 Leu Yyr	(xi) Pro Thr His Asp 50	SEQ Gly Ile Val 35 Met	Pro 20 20 Thr	Ser 5 Ala Asn	SCRI Phe Ser Asp	PTIC Ser Ala Cys Thr	Tyr Ser 40 Pro	Phe Glu 25 Asn Gly	Leu 10 Val Ser Cys	Leu Arg Ser Val	Ala Asn Ile Pro 60	Val Val 45 Cys	Ser 30 Tyr Val	15 Gly Glu Arg	Met Ala Glu		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A	let 1 Leu Tyr 1a	(xi) Pro Thr His Asp 50	SEQ Gly Ile Val 35 Met	Pro 20 20 Thr	Ser 5 Ala Asn	SCRI Phe Ser Asp	PTIC Ser Ala Cys Thr	Tyr Ser 40 Pro	Phe Glu 25 Asn Gly	Leu 10 Val Ser Cys	Leu Arg Ser Val	Ala Asn Ile Pro 60	Val Val 45 Cys	Ser 30 Tyr Val	15 Gly Glu Arg	Met Ala Glu		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204	let 1 Leu Lyr 1a 1sn 65	(xi) Pro Thr His Asp 50 Asn	SEQ Gly Ile Val 35 Met	Pro 20 Thr Ile Ser	CE DE Ser 5 Ala Asn Met	SCRI Phe Ser Asp His Cys 70	PTIC Ser Ala Cys Thr 55	Dein ON: S Ile Tyr Ser 40 Pro Val	Phe Glu 25 Asn Gly Ala	Leu 10 Val Ser Cys Leu	Leu Arg Ser Val Thr 75	Ala Asn Ile Pro 60 Pro	Val Val 45 Cys	Ser 30 Tyr Val Leu	15 Gly Glu Arg Ala	Met Ala Glu Ala 80		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A	let 1 Leu Lyr 1a 1sn 65	(xi) Pro Thr His Asp 50 Asn	SEQ Gly Ile Val 35 Met	Pro 20 Thr Ile Ser	CE DE Ser 5 Ala Asn Met	SCRI Phe Ser Asp His Cys 70	PTIC Ser Ala Cys Thr 55	Dein ON: S Ile Tyr Ser 40 Pro Val	Phe Glu 25 Asn Gly Ala	Leu 10 Val Ser Cys Leu	Leu Arg Ser Val Thr 75	Ala Asn Ile Pro 60 Pro	Val Val 45 Cys	Ser 30 Tyr Val Leu	15 Gly Glu Arg Ala	Met Ala Glu Ala 80		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207	let 1 Leu Lyr 1a 1sn 65	(xi) Pro Thr His Asp 50 Asn	SEQ Gly Ile Val 35 Met Ser	Pro 20 Thr Ile Ser	SE DE Ser 5 Ala Asn Met Arg Val 85	SCRI Phe Ser Asp His Cys 70 Pro	PTIC Ser Ala Cys Thr 55 Trp	tein ON: S Ile Tyr Ser 40 Pro Val	Phe Glu 25 Asn Gly Ala Thr	Leu 10 Val Ser Cys Leu 11e 90	Leu Arg Ser Val Thr 75 Arg	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr	Ser 30 Tyr Val Leu Val	Glu Arg Ala Asp 95	Met Ala Glu Ala 80 Leu		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L	let 1 2yr 1a 1sn 65 1rg	(xi) Pro Thr His Asp 50 Asn Asn	SEQ Gly Ile Val 35 Met Ser Ala	Pro 20 Thr Ile Ser Ser Ala	SE DE Ser 5 Ala Asn Met Arg Val 85 Ala	SCRI Phe Ser Asp His Cys 70 Pro	PTIC Ser Ala Cys Thr 55 Trp Thr	tein DN: S Ile Tyr Ser 40 Pro Val Thr Cys	Phe Glu 25 Asn Gly Ala Thr Ser 105	Leu 10 Val Ser Cys Leu 11e 90 Ala	Leu Arg Ser Val Thr 75 Arg	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr His	Ser 30 Tyr Val Leu Val Gly 110	15 Gly Glu Arg Ala Asp 95 Asp	Met Ala Glu Ala 80 Leu Leu		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L	let 1 2yr 1a 1sn 65 1rg	(xi) Pro Thr His Asp 50 Asn Asn	SEQ Gly Ile Val 35 Met Ser Ala	Pro 20 Thr Ile Ser Ser Ala	SE DE Ser 5 Ala Asn Met Arg Val 85 Ala	SCRI Phe Ser Asp His Cys 70 Pro	PTIC Ser Ala Cys Thr 55 Trp Thr	tein DN: S Ile Tyr Ser 40 Pro Val Thr Cys	Phe Glu 25 Asn Gly Ala Thr Ser 105	Leu 10 Val Ser Cys Leu 11e 90 Ala	Leu Arg Ser Val Thr 75 Arg	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr His	Ser 30 Tyr Val Leu Val Gly 110	15 Gly Glu Arg Ala Asp 95 Asp	Met Ala Glu Ala 80 Leu Leu		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C 213	det 1 Leu 1 leu 1 la 1 l	(xi) Pro Thr His Asp 50 Asn Asn Val	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115	Pro 20 Thr Ile Ser Ser Ala 100 Val	Ser DE Ser 5 Ala Asn Met Arg Val 85 Ala Phe	SCRI Phe Ser Asp His Cys 70 Pro Ala Leu	EPTIC Ser Ala Cys Thr 55 Trp Thr Leu	tein ON: S Ile Tyr Ser 40 Pro Val Thr Cys Ser 120	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala Leu	Leu Arg Ser Val Thr 75 Arg Met Phe	Ala Asn Ile Pro 60 Pro Arg Tyr Thr	Val Val 45 Cys Thr His Val Ile 125	Ser 30 Tyr Val Leu Val Gly 110 Ser	Glu Arg Ala Asp 95 Asp	Met Ala Glu Ala 80 Leu Leu Arg		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C	det 1 Leu 1 Leu 1 Lasn 65 Arg Leu Cys	(xi) Pro Thr His Asp 50 Asn Asn Val	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115	Pro 20 Thr Ile Ser Ser Ala 100 Val	Ser DE Ser 5 Ala Asn Met Arg Val 85 Ala Phe	SCRI Phe Ser Asp His Cys 70 Pro Ala Leu	EPTIC Ser Ala Cys Thr 55 Trp Thr Leu	tein ON: S Ile Tyr Ser 40 Pro Val Thr Cys Ser 120	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala Leu	Leu Arg Ser Val Thr 75 Arg Met Phe	Ala Asn Ile Pro 60 Pro Arg Tyr Thr	Val Val 45 Cys Thr His Val Ile 125	Ser 30 Tyr Val Leu Val Gly 110 Ser	Glu Arg Ala Asp 95 Asp	Met Ala Glu Ala 80 Leu Leu Arg		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C 213 215 A 216	det 1 Leu Lyr Lla Lsn 65 Lrg Leu Leu	(xi) Pro Thr His Asp 50 Asn Val Gly His 130	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115 Glu	Pro 20 Thr Ile Ser Ala 100 Val	Ser 5 Ala Asn Met Arg Val 85 Ala Phe	SCRI Phe Ser Asp His Cys 70 Pro Ala Leu	PTIC Ser Ala Cys Thr 55 Trp Thr Leu Val Asp	Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln Asn	Leu 10 Val Ser Cys Leu 11e 90 Ala Leu Cys	Leu Arg Ser Val Thr 75 Arg Met Phe Ser	Ala Asn Ile Pro 60 Pro Arg Tyr Thr Ile 140	Val Val 45 Cys Thr His Val Ile 125 Tyr	Ser 30 Tyr Val Leu Val Gly 110 Ser	Glu Arg Ala Asp 95 Asp Pro Gly	Met Ala Glu Ala 80 Leu Leu Arg		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C 213 215 A 216 218 I	det 1 Leu Lyr Lla Lsn 65 Lrg Leu Lys Leu Lys	(xi) Pro Thr His Asp 50 Asn Val Gly His 130	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115 Glu	Pro 20 Thr Ile Ser Ala 100 Val	Ser 5 Ala Asn Met Arg Val 85 Ala Phe	SCRIPHE Ser Asp His Cys 70 Pro Ala Leu Gln Met	PTIC Ser Ala Cys Thr 55 Trp Thr Leu Val Asp	Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln Asn	Leu 10 Val Ser Cys Leu 11e 90 Ala Leu Cys	Leu Arg Ser Val Thr 75 Arg Met Phe Ser Met	Ala Asn Ile Pro 60 Pro Arg Tyr Thr Ile 140	Val Val 45 Cys Thr His Val Ile 125 Tyr	Ser 30 Tyr Val Leu Val Gly 110 Ser	Glu Arg Ala Asp 95 Asp Pro Gly	Met Ala Glu Ala 80 Leu Leu Arg His		
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C 213 215 A 216 218 I 219 I	det 1 Leu Lyr Lla Lsn 65 Lrg Leu Lys Leu Lys Lle L45	(xi) Pro Thr His Asp 50 Asn Val Gly His 130 Thr	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115 Glu Gly	Pro 20 Thr Ile Ser Ala 100 Val Thr	CE DE Ser 5 Ala Asn Met Arg Val 85 Ala Phe Val Arg	SCRIPHE Ser Asp His Cys 70 Pro Ala Leu Gln Met 150	PTIC Ser Ala Cys Thr 55 Trp Thr Leu Val Asp 135 Ala	tein ON: S Ile Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys Trp	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln Asn Asp	Leu 10 Val Ser Cys Leu 11e 90 Ala Leu Cys Met	Leu Arg Ser Val Thr 75 Arg Met Phe Ser Met 155	Ala Asn Ile Pro 60 Pro Arg Tyr Thr Ile 140 Met	Val Val 45 Cys Thr His Val Ile 125 Tyr Asn	Ser 30 Tyr Val Leu Val Gly 110 Ser Pro	Glu Arg Ala Asp 95 Asp Pro Gly Ser	Met Ala Glu Ala 80 Leu Leu Arg His Pro 160	,	
189 191 M 192 194 L 195 197 T 198 200 A 201 203 A 204 206 A 207 209 L 210 212 C 213 215 A 216 218 I	det 1 Leu Lyr Lla Lsn 65 Lrg Leu Lys Leu Lys Lle L45	(xi) Pro Thr His Asp 50 Asn Val Gly His 130 Thr	SEQ Gly Ile Val 35 Met Ser Ala Gly Ser 115 Glu Gly	Pro 20 Thr Ile Ser Ala 100 Val Thr	CE DE Ser 5 Ala Asn Met Arg Val 85 Ala Phe Val Arg	SCRIPHE Ser Asp His Cys 70 Pro Ala Leu Gln Met 150	PTIC Ser Ala Cys Thr 55 Trp Thr Leu Val Asp 135 Ala	tein ON: S Ile Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys Trp	Phe Glu 25 Asn Gly Ala Thr Ser 105 Gln Asn Asp	Leu 10 Val Ser Cys Leu 11e 90 Ala Leu Cys Met	Leu Arg Ser Val Thr 75 Arg Met Phe Ser Met 155	Ala Asn Ile Pro 60 Pro Arg Tyr Thr Ile 140 Met	Val Val 45 Cys Thr His Val Ile 125 Tyr Asn	Ser 30 Tyr Val Leu Val Gly 110 Ser Pro	Glu Arg Ala Asp 95 Asp Pro Gly Ser	Met Ala Glu Ala 80 Leu Leu Arg His Pro 160		

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899, 30,3

DATE: 07/20/2001 TIME: 11:23:22

	224 225	Val	Asp	Met	Val 180.		Gly	Ala	His	Trp 185	Gly	Val,	,Leu	Ala	Gly 190	Leu	Ala	
	227 228	Tyr	Tyr	Ser 195			Gly	Asn	Trp 200		Ly.s/	ÝaŽ.	Leu	11e 205	Val	Met	Leu	
		Leu	Phe		T.eu			•	200			_				-		
	231		210		LCu													
		(2)		RMAT	NOI	FOR	SEQ	ID »	rO: 5	i :								
	236		(i)	SEC	QUENC	Œ CE	IARAC	TERI	STIC	S:								
	237		, ,	(P	A) LE	ENGTE	1.:- 79	5 ba	se p	airs	5							
	238				3) TY													
	239			•	C) SI					le			•					
	240			•) TC													
	242		•		LECUI				7									 5, 18, 77
	244	(POTHE			Ю								·		
C>			•		'I-SE		NO											
	249		(1X)		TURE			ana										
	250				A) NA				, 0 2		. **							
	251		/ d \		3) LC		ON:	1/	92.	_								
	253		(1X)		ATURE A) NA		rv.	mat	nent	-ide								
	254				3) LC					Luc								
	255 258		/vi\							EO I	D NC	: 5:						
	250	ΔТС	ጥጥር	CCT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC	TTC	GCC	GAC	CTC	48
	261	Met	T.eu	Glv	Lvs	Val	Tle	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
	262	1	Deu		2,0	5					10	-	-			15		
	264	GTG	GGG	TAC	ATT		CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
	265	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
	266				20					25					30			
	268	GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
	269	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	\mathtt{Tyr}	Ala	
	270			35					40					45				100
	272	ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
	273	Thr	Gly	Asn	Leu	Pro	Gly		Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	274		50					55					60		000		C T C	240
	276	CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG Wal	240
			Ser	Cys	Leu	Thr		Pro	Ala	Ser	Ala		GIU	vaı	Arg	ASII	80	
	278	65					70			03.0	maa	75 mcc	* * * *	mc a	NCC.	አ ጥጥ	_	288
	280	TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	Cor	λen	Sor	Ser	Tle	Val	200
		Ser	GLY	мет	Tyr	HIS	vaı	THE	ASII	ASP	Cys 90	Ser	ASII	361	Jei	95	, 44	
	282	m 3 m	03.0	003	CCC	00	አመረ	አመረግ	አሞሮ	CAC	ACC	CCC	GGG	TGC	GTG		TGC	336
	284	TAT	GAG	Ala	Ala	Acn	Mot	Tla	Mot	His	Thr	Pro	Glv	Cvs	Val	Pro	Cvs	
		TAT	GIU	АІа	100	изр	Mec	116	ric c	105	T ***	110	011	010	110		- 4	
	286	CTT	ccc	CAG	አልሮ	λAC	ሞርሞ	TCC	CGC		TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
	280	Val	Ara	Cli	Agn	Agn	Ser	Ser	Ara	Cvs	Trp	Val	Ala	Leu	Thr	Pro	Thr	
	290	Val	лгу	115	HOH				120	-1-				125				
	292	ርͲሮ	GCA	GCT	AGG	AAC	GCC	AGC		CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432
	293	Len	Ala	Ala	Ara	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
	294		130					135					140					
	274										•							





RAW SEQUENCE LISTING DATE: 07/20/2001 PATENT APPLICATION: US/09/899,303 TIME: 11:23:22

				CTC														480
	145	ASP	ьеи	Leu	vaı	150	АТа	АТа	Ala	File	155	ser	Ala	мес	Tyr			
		GAC	CTC	TGC	CCA		CMC.	ήnα.	CTC	СТС		CAC	CTC	ጥጥር	N.C.C	160		E20
				Cys													-	528
302		ш	пси	Cys	165	JCI	141	- 110	LCu	170	DCI		ساسان ا		175			
	TCG	ССТ	CGC	cGG		GAG	ACG	GTG	CAG		TGC	AAT	TGC	TCA		TAT		576
305	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Cłn	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	,	
306			5	180				_	185	-	-			190		_		
308	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC		624
309	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn.		
310			195					200					205					
				ACA														672
313	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro		
314		210					215					220						
				GTG														720
317	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala		Trp	Gly	Val	Leu		•	
	225					230					235					240		7.00
				TAC														768
	Gly	Leu	Ala	Tyr		Ser	Met	Val	Gly		Trp	Ala	Lys	Val		шe		
322					245					250					255			705
				CTC				'I'AA'I	'AG									795
	Val	Met	Leu	Leu	Phe	Ala	Pro					•						
326		T.1177	> D 2 4 3 6	260		CEO	TD N	10. 4	٠.									
329	(2)	TNE	JKMA.	LTON	FUR	SEU	TD I	VU: ():									
331) SE	QUENC	CE CE	ARAC	CTER	STIC	CS:	ie.								
331 332) SE(QUENC	CE CI ENGTI	HARA(H: 26	CTERI 53 an	ISTIC nino	CS:	is								
331 332 333) SE((<i>1</i> (1	QUENC A) LI B) TY	CE CI ENGTI VPE:	HARA(H: 26 amin	CTERI 53 and a company	ISTIC nino cid	CS:	is								
331 332 333 334		(i)) SE(() () ()	QUENC A) LI B) TY D) TC	CE CI ENGTI (PE: OPOLO	HARAC H: 26 amin DGY:	CTERI 53 an no ac line	ISTIC nino cid ear	CS:	is								
331 332 333 334 336		(ii)) SE(() () () () MO)	QUENC A) LI B) TY D) TC LECUI	CE CHENGTH PE: OPOLO LE TY	HARAC H: 26 amin DGY: YPE:	CTERI 53 an no ac line prot	ISTIC nino cid ear cein	CS: acid		D: 6	:						
331 332 333 334 336 338		(ii)) SE((1 (1 (1)) MO1) SE(QUENC QUENC QUENC QUENC	CE CHENGTHE POLICE TO THE TOTAL POLICE TO THE TOTAL POLICE TO THE TOTAL POLICE	HARAC H: 26 amin DGY: YPE: ESCR	TERI 33 and according 1 incording 1 prot	ISTIC nino cid ear cein ON: S	CS: acid	ID NO): 6 Cys	: Gly	Phe	Ala	Asp	Leu		
331 332 333 334 336 338 340	Met	(ii)) SE((1 (1 (1)) MO1) SE(QUENC A) LI B) TY D) TC LECUI	CE CHENGTHE POLICE TO THE TOTAL POLICE TO THE TOTAL POLICE TO THE TOTAL POLICE	HARAC H: 26 amin DGY: YPE: ESCR	TERI 33 and according 1 incording 1 prot	ISTIC nino cid ear cein ON: S	CS: acid	ID NO): 6 Cys	: Gly	Phe	Ala	Asp 15	Leu		
331 332 333 334 336 338 340 341	Met 1	(ii (xi Leu) SE((1 (1) MO1) SE(Gly	Lys Lys	CE CIENGTI OPOLO LE TY CE DI Val	HARAC H: 26 amin DGY: YPE: ESCRI	CTERI 63 am no ac line prot PTIC Asp	ISTIC nino cid ear cein ON: S	ES: acid SEQ : Leu	ID NO Thr 10	Cys	Gly			15			
331 332 333 334 336 338 340 341	Met 1	(ii (xi Leu) SE((1 (1) MO1) SE(Gly	QUENC QUENC QUENC QUENC	CE CIENGTI OPOLO LE TY CE DI Val	HARAC H: 26 amin DGY: YPE: ESCRI	CTERI 63 am no ac line prot PTIC Asp	ISTIC nino cid ear cein ON: S	ES: acid SEQ : Leu	ID NO Thr 10	Cys	Gly			15			
331 332 333 334 336 338 340 341 343	Met 1 Val	(ii (xi Leu Gly) SE((1 (1)) MO1) SE(Gly	QUENCA) LH B) TY D) TC LECUI QUENC LYS Ile 20	CE CHENGTH VPE: DPOLC LE TY CE DI Val Pro	HARAC H: 26 amin DGY: YPE: ESCR: Ile Leu	CTERN 53 am no ac line prot PTIC Asp	ISTIC nino cid ear cein ON: S Thr	SEQ Leu Ala 25	ID NO Thr 10 Pro	Cys Leu	Gly Gly	Gly	Ala 30	15 Ala	Arg		
331 332 333 334 336 340 341 343 344 346 347	Met 1 Val	(ii (xi Leu Gly) SE() (1 (1) (1) MOI) SE() Gly Tyr Ala 35	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His	CE CHENGTH VPE: DPOLO LE TY CE DI Val 5 Pro	HARACH: 26 amin DGY: YPE: ESCRI Ile Leu Val	CTERD 53 am no ac line prot IPTIC Asp Val	ISTIC mino cid ear cein DN: S Thr Gly Val	SEQ I Leu Ala 25 Leu	ID NO Thr 10 Pro Glu	Cys Leu Asp	Gly Gly Gly	Gly Val 45	Ala 30 Asn	15 Ala Tyr	Arg Ala		
331 332 333 334 336 340 341 343 344 346 347	Met 1 Val	(ii (xi Leu Gly) SE() (1 (1) (1) MOI) SE() Gly Tyr Ala 35	QUENCA) LH B) TY D) TC LECUI QUENC LYS Ile 20	CE CHENGTH VPE: DPOLO LE TY CE DI Val 5 Pro	HARACH: 26 amin DGY: YPE: ESCRI Ile Leu Val	CTERD 53 am no ac line prot IPTIC Asp Val	ISTIC mino cid ear cein DN: S Thr Gly Val	SEQ I Leu Ala 25 Leu	ID NO Thr 10 Pro Glu	Cys Leu Asp	Gly Gly Gly	Gly Val 45	Ala 30 Asn	15 Ala Tyr	Arg Ala		
331 332 333 334 336 348 341 343 344 346 347 349 350	Met 1 Val Ala Thr	(ii) (xi) Leu Gly Leu Gly 50	() SEQ (1) (1) MOI () SEQ Gly Tyr Ala 35 Asn	QUENCA) LH B) TY C) TC LECUI QUENC LYS Ile 20 His	CE CE ENGTH YPE: DPOLO LE TY CE DI Val 5 Pro Gly	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly	CTERNO 3 am no according protection Asp Val Arg Cys 55	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser	SEQ I Leu Ala 25 Leu Phe	ID NO Thr 10 Pro Glu Ser	Cys Leu Asp Ile	Gly Gly Gly Phe 60	Gly Val 45 Leu	Ala 30 Asn Leu	15 Ala Tyr Ala	Arg Ala Leu		
331 332 333 334 336 348 341 343 344 346 347 349 350	Met 1 Val Ala Thr	(ii) (xi) Leu Gly Leu Gly 50	() SEQ (1) (1) MOI () SEQ Gly Tyr Ala 35 Asn	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His	CE CE ENGTH YPE: DPOLO LE TY CE DI Val 5 Pro Gly	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly	CTERNO 3 am no according protection Asp Val Arg Cys 55	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser	SEQ I Leu Ala 25 Leu Phe	ID NO Thr 10 Pro Glu Ser	Cys Leu Asp Ile	Gly Gly Gly Phe 60	Gly Val 45 Leu	Ala 30 Asn Leu	15 Ala Tyr Ala	Arg Ala Leu Val		
331 332 333 334 336 338 340 341 343 344 346 347 349 350 352 353	Met 1 Val Ala Thr Leu 65	(ii (xi Leu Gly Leu Gly 50 Ser	() SE() (1) (1) MOD (1) SE() Gly Tyr Ala 35 Asn Cys	QUENCA) LIB B) TY C) TC LECUI QUENC LYS Ile 20 His Leu Leu	CE CE ENGTH VPE: DPOLO LE TY CE DI Val 5 Pro Gly Pro	HARACH: 26 amin DGY: VPE: ESCR: Ile Leu Val Gly Val 70	CTERION STATE OF THE PROPERTY	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser	SEQ : Leu Ala 25 Leu Phe Ser	ID NO Thr 10 Pro Glu Ser	Cys Leu Asp Ile Tyr 75	Gly Gly Gly Phe 60 Glu	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn	Arg Ala Leu Val 80		
331 332 333 334 336 338 340 341 343 344 346 347 349 350 352 353	Met 1 Val Ala Thr Leu 65	(ii (xi Leu Gly Leu Gly 50 Ser	() SE() (1) (1) MOD (1) SE() Gly Tyr Ala 35 Asn Cys	QUENCA) LH B) TY C) TC LECUI QUENC LYS Ile 20 His	CE CE ENGTH VPE: DPOLO LE TY CE DI Val 5 Pro Gly Pro	HARACH: 26 amin DGY: VPE: ESCR: Ile Leu Val Gly Val 70	CTERION STATE OF THE PROPERTY	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser	SEQ : Leu Ala 25 Leu Phe Ser	Thr 10 Pro Glu Ser Ala	Cys Leu Asp Ile Tyr 75	Gly Gly Gly Phe 60 Glu	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn Ile	Arg Ala Leu Val 80		
331 332 333 334 336 341 343 344 346 347 349 350 352 353 355 356	Met 1 Val Ala Thr Leu 65 Ser	(ii (xi Leu Gly Leu Gly 50 Ser	() SE() (1) (1) (1) (1) (1) (2) (3) (4) (4) (5) (6) (7) (7) (7) (8) (9) (9) (9) (9) (9) (10) (10) (10) (10) (10) (10) (10) (10	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His Leu Leu Tyr	CE CHENGTH VPE: OPOLO LE TY CE DI Val Fro Gly Pro Thr His	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly Val 70 Val	CTERNO 3 am no according protection of the prote	STIC nino cid ear cein ON: S Thr Gly Val 40 Ser Ala	SEQ Leu Ala 25 Leu Phe Ser Asp	ID NO Thr 10 Pro Glu Ser Ala Cys 90	Cys Leu Asp Ile Tyr 75 Ser	Gly Gly Gly Phe 60 Glu Asn	Gly Val 45 Leu Val Ser	Ala 30 Asn Leu Arg Ser	15 Ala Tyr Ala Asn Ile 95	Arg Ala Leu Val 80 Val		
331 332 333 334 336 340 341 343 344 346 347 349 350 352 353 355 356 358	Met 1 Val Ala Thr Leu 65 Ser	(ii (xi Leu Gly Leu Gly 50 Ser	() SE() (1) (1) (1) (1) (1) (2) (3) (4) (4) (5) (6) (7) (7) (7) (8) (9) (9) (9) (9) (9) (10) (10) (10) (10) (10) (10) (10) (10	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His Leu Leu Tyr Ala	CE CHENGTH VPE: OPOLO LE TY CE DI Val Fro Gly Pro Thr His	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly Val 70 Val	CTERNO 3 am no according protection of the prote	STIC nino cid ear cein ON: S Thr Gly Val 40 Ser Ala	SEQ Leu Ala 25 Leu Phe Ser Asp	ID NO Thr 10 Pro Glu Ser Ala Cys 90	Cys Leu Asp Ile Tyr 75 Ser	Gly Gly Gly Phe 60 Glu Asn	Gly Val 45 Leu Val Ser	Ala 30 Asn Leu Arg Ser	15 Ala Tyr Ala Asn Ile 95	Arg Ala Leu Val 80 Val		
331 332 333 334 336 341 343 344 346 347 349 350 352 353 355 356 358 359	Met 1 Val Ala Thr Leu 65 Ser	(ii (xi Leu Gly Leu Gly 50 Ser Gly	() SEQ (1) (1) MOI () SEQ Gly Tyr Ala 35 Asn Cys Met	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His Leu Tyr Ala 100	CE CHENGTH VPE: DPOLO LE TY Val 5 Pro Gly Pro Thr His 85 Asp	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly Val 70 Val Met	CTERION STATE OF THE TITE OF T	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser Ala Asn	SEQ Leu Ala 25 Leu Phe Ser Asp His	ID NO Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro	Gly Gly Phe 60 Glu Asn Gly	Gly Val 45 Leu Val Ser Cys	Ala 30 Asn Leu Arg Ser Val 110	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys		
331 332 333 334 336 340 341 343 344 346 347 352 353 355 356 358 359 361	Met 1 Val Ala Thr Leu 65 Ser	(ii (xi Leu Gly Leu Gly 50 Ser Gly	() SEQ (1) (1) (1) MOD (1) SEQ Gly Tyr Ala 35 Asn Cys Met Ala Glu	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His Leu Leu Tyr Ala	CE CHENGTH VPE: DPOLO LE TY Val 5 Pro Gly Pro Thr His 85 Asp	HARACH: 26 amin DGY: VPE: ESCRI Ile Leu Val Gly Val 70 Val Met	CTERION STATE OF THE TITE OF T	ISTIC mino cid ear cein ON: S Thr Gly Val 40 Ser Ala Asn Met	SEQ Leu Ala 25 Leu Phe Ser Asp His	ID NO Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro	Gly Gly Phe 60 Glu Asn Gly	Gly Val 45 Leu Val Ser Cys Leu	Ala 30 Asn Leu Arg Ser Val 110	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys		
331 332 333 334 336 340 341 343 344 346 347 349 350 352 353 355 356 358 359 361 362	Met 1 Val Ala Thr Leu 65 Ser Tyr	(ii (xi Leu Gly 50 Ser Gly Glu Arg	() SEQ (1) (1) (1) MOD (1) SEQ (1) Gly Tyr Ala 35 Asn Cys Met Ala Glu 115	QUENCA) LH B) TY C) TO LECUI QUENC Lys Ile 20 His Leu Tyr Ala 100 Asn	CE CHENGTH VPE: DPOLO LE TY Val 5 Pro Gly Pro Thr His 85 Asp	HARACH: 26 amin DGY: YPE: ESCRITE Leu Val Gly Val Met Ser	CTERNO 3 am no according protection of the prote	ISTIC nino cid ear cein ON: S Thr Gly Val 40 Ser Ala Asn Met	SEQ Deu Ala 25 Leu Phe Ser Asp His 105 Cys	ID NO Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro Val	Gly Gly Phe 60 Glu Asn Gly Ala	Gly Val 45 Leu Val Ser Cys Leu 125	Ala 30 Asn Leu Arg Ser Val 110 Thr	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys		
331 332 333 334 336 340 341 343 344 346 347 349 350 352 353 355 356 358 359 361 362	Met 1 Val Ala Thr Leu 65 Ser Tyr	(ii (xi Leu Gly 50 Ser Gly Glu Arg	() SEQ (1) (1) (1) MOD (1) SEQ (1) Gly Tyr Ala 35 Asn Cys Met Ala Glu 115	QUENCA) LH B) TY C) TC LECUI QUENC Lys Ile 20 His Leu Tyr Ala 100	CE CHENGTH VPE: DPOLO LE TY Val 5 Pro Gly Pro Thr His 85 Asp	HARACH: 26 amin DGY: YPE: ESCRITE Leu Val Gly Val Met Ser	CTERNO 3 am no according protection of the prote	ISTIC nino cid ear cein ON: S Thr Gly Val 40 Ser Ala Asn Met	SEQ Deu Ala 25 Leu Phe Ser Asp His 105 Cys	ID NO Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro Val	Gly Gly Phe 60 Glu Asn Gly Ala	Gly Val 45 Leu Val Ser Cys Leu 125	Ala 30 Asn Leu Arg Ser Val 110 Thr	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys		

VERIFICATION SUMMARY DATE: 07/20/2001 PATENT APPLICATION: US/09/899,303 TIME: 11:23:23

```
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:66 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:87 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:109 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:246 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:404 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:541 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:649 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:758 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:916 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:936 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:956 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:976 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:996 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1016 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1088 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1160 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1283 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1413 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1550 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1686 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1823 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1843 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1863 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2118 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2310 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2503 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2681 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2861 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3103 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3449 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:4729 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4749 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4771 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4792 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4812 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4832 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4852 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4872 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4892 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4912 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:4952 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
```

VERIFICATION SUMMARYDATE: 07/20/2001PATENT APPLICATION: US/09/899,303TIME: 11:23:23

L:4972	M:220	C :	Keyword	misspelled	or	invalid	format,	(iv)	ANTI-SENSE:]
L:4992	M:220	C:	Keyword	misspelled	or	invalid	format,	(iv)	ANTI-SENSE:]
L:5012	M:220	C:	Keyword	misspelled	or	invalid	format,	((iv)	ANTI-SENSE:]
L:5032	M:220	C:	Keyword	${\tt misspelled}$	or	invalid	format,	((iv)	ANTI-SENSE:]
L:5052	M:220	C:	Keyword	misspelled	or	invalid	format,	(iv)	ANTI-SENSE:]
L:5072	M:220	C:	Keyword	misspelled	or	invalid	format,	(iv)	ANTI-SENSE:]